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(21) International Application Number: PCT/US98/00359 (22) International Filing Date: 9 January 1998 (09.01.98) (30) Priority Data: 60/035,560 14 January 1997 (14.01.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/035,560 (CON) Filed on 14 January 1997 (14.01.97) (71)(72) Applicants and Inventors: JAYNE, Susan [US/US]; 4334 Woodland Avenue, Des Moines, IA 50312 (US). BARBOUR, Eric [US/US]; 6700 N.W. Timberline Drive, Des Moines, IA 50313 (US). (72) Inventor; and (75) Inventor/Applicant: MEYER, Terry (74) Agents: SPRUILL, W., Murray et al.; Bell Seltzer Intellectual Property Law Group, Alston & Bird LLP, P.O. Drawer 34009, Charlotte, NC 28234 (US).		(81) Designated States: AL, AM, AT, AT (Utility model), AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), EE, EE (Utility model), ES, FI, FI (Utility model), GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: METHODS FOR IMPROVING TRANSFORMATION EFFICIENCY (57) Abstract The present invention is drawn to compositions and methods for improving transformation efficiency. The compositions, synthetic marker genes, are used in transformation methods and result in increased transformation efficiency. The synthetic marker genes can be designed for maximum expression in any system.		

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METHODS FOR IMPROVING TRANSFORMATION EFFICIENCY

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a Continuation-In-Part of Provisional application Serial No. 60/035,560 filed January 14, 1997.

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FIELD OF THE INVENTION

The invention relates to the genetic modification of organisms, particularly plants.

BACKGROUND OF THE INVENTION

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Gene transfer has offered great promise in the genetic manipulation of organisms. The movement of genes within plant species has played an important role in crop improvement for many decades. The recombinant DNA methods which have been developed have greatly extended the sources from which genetic information can be obtained for crop improvement. Gene transfer systems based on recombinant DNA are available for several crop species and are under development for many others.

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Rapid progress has been made in developing the tools for manipulating genetic information in plants. Plant genes are being cloned, genetic regulatory signals deciphered, and genes transferred from entirely unrelated organisms to confer new agriculturally useful traits to crop plants. Recombinant DNA methods significantly increase the gene pool available for crop improvement.

A variety of methods have been developed for the transformation of plants and plant cells with DNA. Generally, the most success has been in dicotyledonous plants. Some success has been reported with certain monocotyledonous cereals.

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Cereals comprise a commercially valuable group of plant species that could benefit from the introduction and expression of foreign genes controlling improved grain quality and such agronomically important traits as tolerance to disease, insects, herbicides, and stress. However, most cereals have not proven readily amenable to either *Agrobacterium*-mediated gene delivery, or to the routine regeneration of fertile transgenic plants from directly transformed protoplasts. The use of microprojectile-bombardment-mediated transformation of embryogenic tissue culture material, with the subsequent regeneration of transgenic plants, has overcome the regeneration problems associated with the production of plants from cereal protoplasts. Using this technology, transgenic plants have been obtained from microprojectile-bombarded tissue cultures of many species.

Many of the recent advances in plant science have resulted from application of the analytical power of recombinant DNA technology coupled with plant transformation. These approaches facilitate studies of the effects of specific gene alterations and additions on plant development and physiology. They also make possible the direct manipulation of genes to bio-engineer improved plant varieties.

While strides have been made in the genetic transformation of plants, it is by no means a routine matter. In fact, transformation efficiency is quite low making the process very labor intensive. Some reports indicate that the current transformation methods provide only a transformation frequency of about one event from every thousand bombarded embryos. This transformation frequency is too low for many genetic studies and for routine commercial applications. Therefore, a method is needed to improve the efficiency of genetic transformation.

SUMMARY OF THE INVENTION

Compositions and methods for improving transformation efficiency in organisms, particularly plants, are provided. The compositions, synthetic marker genes, are used in transformation methods and result in increased transformation efficiency. The synthetic marker genes can be designed for maximum expression in any system.

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DESCRIPTION OF THE FIGURES

Figure 1: Nucleotide sequence of phosphinothricin acetyltransferase optimized for expression in monocots.

5 Figure 2: Nucleotide sequence of cyanamide hydratase optimized for expression in monocots.

DETAILED DESCRIPTION OF THE INVENTION

10 The present invention is drawn to compositions and methods for improving transformation efficiency in organisms, particularly plants. For use in plants, the method involves stably transforming a plant cell or culture and regenerating plants from the transformed cells. Using the methods of the invention, fertile transgenic plants can be grown to maturity with a high frequency. The fertile transformed plants are capable of producing transformed progeny that express foreign genes of
15 interest.

 The methods of the present invention improve transformation efficiency. By improve efficiency it is intended that the number of transformed plants recovered by a transformation attempt is increased preferably at least two fold, preferably at least five fold, more preferably at least ten fold.

20 The present invention thus encompasses the fertile transgenic plants and transformed seeds thereof, as well as the subsequent progeny and products derived therefrom.

 By transformation is intended the genetic manipulation of the plant, cell, cell line, callus, tissue, plant part, and the like. That is, such cell, cell line, callus,
25 tissue, plant part, or plant which has been altered by the presence of recombinant DNA wherein said DNA is introduced into the genetic material within the cell, either chromosomally, or extra-chromosomally. Recombinant DNA includes foreign DNA, heterologous DNA, exogenous DNA, and chimeric DNA.

 The transformed plants of the invention can be produced by genetic
30 engineering. Alternatively, transformed parent plants can be produced by genetic

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engineering and used to transfer the foreign genes into subsequent generations by sexual or asexual reproduction.

The methods of the present invention can be used in combination with any means for transformation of plants or plant cells. The present invention provides for the use of an optimized marker gene. The marker gene can be optimized for expression in a particular plant species, a particular genus of plants or a particular group of plants, for example monocots and/or dicots, maize, wheat, soybean, and the like.

By marker gene is intended both selectable marker genes and reporter genes. Both selectable marker genes and reporter genes facilitate identification and selection of transformed cells. To date, all genetic transformation systems which have been developed rely upon a selectable marker or reporter gene to enable the recovery of transgenic plants.

Reporter genes should ideally exhibit low background activity and should not have any detrimental effects on metabolism. The reporter gene products will have moderate stability *in vivo*, so that down-regulation of gene expression as well as gene activity can be detected. Finally, the reporter gene should be able to be assayed by a non-destructive, quantitative, sensitive, simple to perform and inexpensive system.

Reporter genes are known in the art and include but are not limited to: Beta-glucuronidase (GUS) gene (Jefferson *et al.* (1991) *In Plant Molecular Biology Manual* (Gelvin *et al.*, eds.), pp. 1-33, Kluwer Academic Publishers). This gene is encoded by the *uidA* locus of *E. coli*. GUS enzyme activity can be assayed easily and sensitively in plants. The expression of GUS gene fusions can be quantified by fluorometric assay, and histochemical analysis can be used to localize gene activity in transgenic tissues.

Luciferase (DeWet *et al.* (1987) *Mol. Cell. Biol.*, 7:725-737). Luciferase catalyzes the oxidation of D(-)-luciferin in the presence of ATP to generate oxyluciferin and yellow-green light.

Anthocyanins (Goff *et al.* (1990) *EMBO J.*, 9:2517-2522). Anthocyanin is a reporter system that does not require the application of external substrates for its

detection. The anthocyanin system utilizes the C1, B and R genes, which code for trans-acting factors that regulate the anthocyanin biosynthetic pathway in maize seeds. The introduction of these regulatory genes under the control of constitutive promoters includes cell-autonomous pigmentation in non-seed tissues.

5 Green fluorescent protein (GFP) from the jellyfish *Aequorea victoria* (Kain *et al.* (1995) *BioTechniques*, 19:650-655 and Chiu *et al.* (1996) *Current Biology*, 6:325-330). GFP emits bright green light when excited with UV or blue light. GFP fluorescence does not require a substrate or cofactor, is stable, and can be monitored non-invasively in living cells.

10 Selectable marker genes are utilized for the selection of transformed cells or tissues. Selectable marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (*NEO*) and hygromycin phosphotransferase (*HPT*) as well as genes conferring resistance to herbicidal compounds. Herbicide resistance genes generally code for a modified target protein
15 insensitive to the herbicide or for an enzyme that degrades or detoxifies the herbicide in the plant before it can act. (See DeBlock *et al.* (1987) *EMBO J.*, 6:2513-2518; DeBlock *et al.* (1989) *Plant Physiol.*, 91:691-704; Fromm *et al.* (1990) 8:833-839; Gordon-Kamm *et al.* (1990) 2:603-618) For example, resistance to glyphosate or sulfonylurea herbicides has been obtained by using genes coding
20 for the mutant target enzymes, 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) and acetolactate synthase (ALS). Resistance to glufosinate ammonium, bromoxynil, and 2,4-dichlorophenoxyacetate (2,4-D) have been obtained by using bacterial genes encoding phosphinothricin acetyltransferase, a nitrilase, or a 2,4-dichlorophenoxyacetate monooxygenase, which detoxify the respective herbicides.

25 For purposes of the present invention, selectable marker genes include, but are not limited to genes encoding: neomycin phosphotransferase II (Fraley *et al.* (1986) *CRC Critical Reviews in Plant Science*, 4:1-25); cyanamide hydratase (Maier-Greiner *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:4250-4264); aspartate kinase; dihydrodipicolinate synthase (Perl *et al.* (1993) *Bio/Technology*, 11:715-
30 718); tryptophan decarboxylase (Goddijn *et al.* (1993) *Plant Mol. Bio.*, 22:907-912); dihydrodipicolinate synthase and desensitized aspartate kinase (Perl *et al.*

(1993) *Bio/Technology*, 11:715-718); bar gene (Toki *et al.* (1992) *Plant Physiol.*, 100:1503-1507 and Meagher *et al.* (1996) and *Crop Sci.*, 36:1367); tryptophan decarboxylase (Goddijn *et al.* (1993) *Plant Mol. Biol.*, 22:907-912); neomycin phosphotransferase (NEO) (Southern *et al.* (1982) *J. Mol. Appl. Gen.*, 1:327;
5 hygromycin phosphotransferase (HPT or HYG) (Shimizu *et al.* (1986) *Mol. Cell Biol.*, 6:1074); dihydrofolate reductase (DHFR) (Kwok *et al.* (1986) *PNAS USA* 4552); phosphinothricin acetyltransferase (DeBlock *et al.* (1987) *EMBO J.*, 6:2513); 2,2-dichloropropionic acid dehalogenase (Buchanan-Wollaston *et al.* (1989) *J. Cell. Biochem.* 13D:330); acetohydroxyacid synthase (Anderson *et al.*,
10 U.S. Patent No. 4,761,373; Haughn *et al.* (1988) *Mol. Gen. Genet.* 221:266); 5-enolpyruvyl-shikimate-phosphate synthase (aroA) (Comai *et al.* (1985) *Nature* 317:741); haloarylnitrilase (Stalker *et al.*, published PCT applcn WO87/04181); acetyl-coenzyme A carboxylase (Parker *et al.* (1990) *Plant Physiol.* 92:1220); dihydropteroate synthase (sul I) (Guerineau *et al.* (1990) *Plant Mol. Biol.* 15:127);
15 32 kD photosystem II polypeptide (psbA) (Hirschberg *et al.* (1983) *Science*, 222:1346); etc.

Also included are genes encoding resistance to: chloramphenicol (Herrera-Estrella *et al.* (1983) *EMBO J.*, 2:987-992); methotrexate (Herrera-Estrella *et al.* (1983) *Nature*, 303:209-213; Meijer *et al.* (1991) *Plant Mol Bio.*, 16:807-820
20 (1991); hygromycin (Waldron *et al.* (1985) *Plant Mol. Biol.*, 5:103-108; Zhijian *et al.* (1995) *Plant Science*, 108:219-227 and Meijer *et al.* (1991) *Plant Mol. Bio.* 16:807-820); streptomycin (Jones *et al.* (1987) *Mol. Gen. Genet.*, 210:86-91); spectinomycin (Bretagne-Sagnard *et al.* (1996) *Transgenic Res.*, 5:131-137); bleomycin (Hille *et al.* (1986) *Plant Mol. Biol.*, 7:171-176); sulfonamide
25 (Guerineau *et al.* (1990) *Plant Mol. Bio.*, 15:127-136); bromoxynil (Stalker *et al.* (1988) *Science*, 242:419-423); 2,4-D (Streber *et al.* (1989) *Bio/Technology*, 7:811-816); glyphosate (Shaw *et al.* (1986) *Science*, 233:478-481); phosphinothricin (DeBlock *et al.* (1987) *EMBO J.*, 6:2513-2518).

See generally, G. T. Yarranton (1992) *Curr. Opin. Biotech.*, 3:506-511;
30 Christopherson *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:6314-6318; Yao *et al.* (1992) *Cell*, 71:63-72; W. S. Reznikoff (1992) *Mol. Microbiol.*, 6:2419-2422;

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Barkley *et al.* (1980) *The Operon*, pp. 177-220; Hu *et al.* (1987) *Cell*, 48:555-566; Brown *et al.* (1987) *Cell*, 49:603-612; Figge *et al.* (1988) *Cell*, 52:713-722; Deuschle *et al.* (1989) *Proc. Natl. Acad. Sci. USA*, 86:5400-5404; Fuerst *et al.* (1989) *Proc. Natl. Acad. Sci. USA*, 86:2549-2553; Deuschle *et al.* (1990) *Science*, 248:480-483; M. Gossen (1993) PhD Thesis, University of Heidelberg; Reines *et al.* (1993) *Proc. Natl. Acad. Sci. USA*, 90:1917-1921; Labow *et al.* (1990) *Mol. Cell Bio.*, 10:3343-3356; Zambretti *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:3952-3956; Baim *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:5072-5076; Wyborski *et al.* (1991) *Nuc. Acids Res.*, 19:4647-4653; A. Hillenand-Wissman (1989) *Topics in Mol. and Struc. Biol.*, 10:143-162; Degenkolb *et al.* (1991) *Antimicrob. Agents Chemother.*, 35:1591-1595; Kleinschmidt *et al.* (1988) *Biochemistry*, 27:1094-1104; Gatz *et al.* (1992) *Plant J.*, 2:397-404; A. L. Bonin (1993) PhD Thesis, University of Heidelberg; Gossen *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:5547-5551; Oliva *et al.* (1992) *Antimicrob. Agents Chemother.*, 36:913-919; Hlavka *et al.* (1985) *Handbook of Exp. Pharmacology*, 78; Gill *et al.* (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference.

The above list of selectable marker and reporter genes are not meant to be limiting. Any reporter or selectable marker gene are encompassed by the present invention. If necessary, such genes can be sequenced by methods known in the art.

The reporter and selectable marker genes are synthesized for optimal expression in the plant. That is, the coding sequence of the gene has been modified to enhance expression in plants. The synthetic marker gene is designed to be expressed in plants at a higher level resulting in higher transformation efficiency.

Methods for synthetic optimization of genes are available in the art. In fact, several genes have been optimized to increase expression of the gene product in plants. However, until the present invention no one had recognized that transformation efficiency could be improved by genetic modification of the marker gene for optimal expression in the cell being transformed.

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The marker gene sequence can be optimized for expression in a particular plant species or alternatively can be modified for optimal expression in plant families. The plant preferred codons may be determined from the codons of highest frequency in the proteins expressed in the largest amount in the particular plant species of interest. See, for example, EPA 0359472; EPA 0385962; WO 91/16432; 5 Perlak *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:3324-3328; and Murray *et al.* (1989) *Nucleic Acids Research*, 17: 477-498. U.S. Patent No. 5,380,831; U.S. Patent No. 5,436,391; and the like, herein incorporated by reference. In this manner, the nucleotide sequences can be optimized for expression in any plant. It 10 is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, fully optimized or partially optimized sequences may also be used.

In the same manner, genes can be optimized for expression in any organism. Thus, while the invention is described in relation to improving the transformation efficiency in plants, the methods of the invention can be applied to improving the 15 transformation efficiency in any system.

The marker genes of the invention are provided in expression cassettes for expression in the organism of interest. In this manner, the cassette will include 5' and 3' regulatory sequences operably linked to the gene of interest. Additionally, 20 the expression cassette may be linked at the 5' end to various promoters from the same or different organisms. These promoters would be selected for strength and/or inducibility. Examples of such promoters include but are not limited to the ubiquitin-1 (Ubi-1) promoter or the cauliflower mosaic virus 35S (CaMv) promoter. See for example Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689; Cornijo *et al.* 25 *et al.* (1993) *Plant Mol. Biol.* 23:567-581; Hohn *et al.* (1993) *PNAS* 93(16):8334-8339. The expression cassette may also include 3' terminator regions linked to the gene of interest examples of which are the CaMV 35S terminator and the potato proteinase inhibitor protein or pin II terminator. See for example, Mitsuhara *et al.* (1996) *Plant Cell Physiol.* 37(1):49-59; Seymour *et al.* (1993) *Plant Mol. Biol.* 30 23(1):1-9; The cassette may additionally contain at least one gene to be cotransformed into the organism. Alternatively, the additional gene(s) of interest

can be provided on another expression cassette. Where appropriate, the additional gene(s) of interest may be optimized for increased expression in the transformed plant.

5 The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein, O., Fuerst, T.R., and Moss, B. (1989) *PNAS USA*, 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.* (1986);
10 MDMV leader (Maize Dwarf Mosaic Virus); *Virology*, 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP), (Macejak, D.G., and P. Sarnow (1991) *Nature*, 353:90-94; untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling, S.A., and Gehrke, L., (1987) *Nature*, 325:622-625; tobacco mosaic virus leader (TMV), (Gallie, D.R. *et al.*
15 (1989) *Molecular Biology of RNA*, pages 237-256; and maize chlorotic mottle virus leader (MCMV) (Lommel, S.A. *et al.* (1991) *Virology*, 81:382-385). See also, Della-Cioppa *et al.* (1987) *Plant Physiology*, 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be
20 manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate in the proper reading frame. Towards this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis,
25 primer repair, restriction, annealing, resection, ligation, PCR, or the like may be employed, where insertions, deletions or substitutions, *e.g.* transitions and transversions, may be involved.

The compositions and methods of the present invention can be used in any transformation protocol. Such transformation protocols may vary depending on the
30 type of plant or plant cell, *i.e.* monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection (Crossway *et al.*

(1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA*, 83:5602-5606, *Agrobacterium* mediated transformation (Hinchee *et al.* (1988) *Biotechnology*, 6:915-921), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.*, 3:2717-2722), and ballistic particle acceleration (see, for example, Sanford *et al.*, U.S. Patent 4,945,050; WO91/10725 and McCabe *et al.* (1988) *Biotechnology*, 6:923-926). Also see, Weissinger *et al.* (1988) *Annual Rev. Genet.*, 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology*, 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674(soybean); McCabe *et al.* (1988) *Bio/Technology*, 6:923-926 (soybean); Datta *et al.* (1990) *Biotechnology*, 8:736-740(rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA*, 85:4305-4309 (maize); Klein *et al.* (1988) *Biotechnology*, 6:559-563 (maize); WO91/10725 (maize); Klein *et al.* (1988) *Plant Physiol.*, 91:440-444(maize); Fromm *et al.* (1990) *Biotechnology*, 8:833-839; and Gordon-Kamm *et al.* (1990) *Plant Cell*, 2:603-618 (maize); Hooydaas-Van Slogteren & Hooykaas (1984) *Nature* (London), 311:763-764; Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA*, 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) In *The Experimental Manipulation of Ovule Tissues*, ed. G.P. Chapman *et al.*, pp. 197-209. Longman, NY (pollen); Kaeppler *et al.* (1990) *Plant Cell Reports*, 9:415-418; and Kaeppler *et al.* (1992) *Theor. Appl. Genet.*, 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell*, 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant Cell Reports*, 12:250-255 and Christou and Ford (1995) *Annals of Botany*, 75:407-413 (rice); Osjoda *et al.* (1996) *Nature Biotechnology*, 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

The plant plastid can also be transformed directly. Stable transformation of plastids have been reported in higher plants. See, for example, Svab *et al.* (1990) *Proc. Nat'l. Acad. Sci. USA*, 87:8526-8530; Svab & Maliga (1993) *Proc. Nat'l. Acad. Sci. USA*, 90:913-917; Svab & Maliga (1993) *EMBO J.*, 12:601-606. The method relies on particular gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by trans-activation of a silent plastid-borne transgene by tissue-specific expression of a nuclear-encoded and

plastid-directed RNA polymerase. Such a system has been reported in McBride *et al.* (1994) *Proc. Natl. Acad. Sci., USA*, 91:7301-7305. Where the transformation protocol is directed to plastid transformation, the marker genes are optimized for expression in the plant plastid.

5 The cells which have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Reports*, 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having the desired phenotypic characteristic identified. Two or more generations
10 may be grown to ensure that the subject phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure the desired phenotype or other property has been achieved.

While the present method has broad applicability, it is particularly useful in transforming plants which have been recalcitrant to known transformation methods. That is using the present method, maize elite lines, inbreds, and other lines difficult to transform can be transformed directly.

The following examples are offered by way of illustration and not by way of limitation.

20 **EXPERIMENTAL**

EXAMPLE I. GENERATION OF A MONOCOT-OPTIMIZED PAT GENE

The PAT gene, which confers resistance to the herbicide glufosinate ammonium, was originally cloned from *Streptomyces viridochromogenes*. The plasmid pB2/35S Δ CK consists of a synthetic plant-optimized PAT gene fused to a 35S-promoter and terminator cloned into pUC19. A second construct consisting of the PAT gene fused to a plant ubiquitin promoter was also utilized.

The PAT gene was first modified for expression in plants by replacing the GTG codon with ATG, and by modifying the four nucleotides upstream of the ATG codon to generate a plant-optimized PAT gene. The present invention relates to the further modification of the PAT gene to generate an example of a monocot-optimized selectable marker gene, the "monocot-optimized" PAT gene (moPAT).

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Analysis of the success of monocot-optimization was determined by recovery of transformants when the monocot-optimized PAT gene was used as a selectable marker, resulting in the isolation of a large number of highly herbicide-resistant events.

5 In order to generate a monocot-optimized form of the PAT gene, the preferred codon usage patterns for maize were examined. See, for example, Adang, U.S. Patent No. 5,380,831. Information regarding the preferred codon usage of maize allowed for the replacement of codons with those codons that were more frequently used in maize. Codons were altered without altering the amino
10 acid sequence of the PAT polypeptide. A codon usage table that reflects the codon usage of the monocot *Zea mays* was utilized to optimize the PAT gene expression in monocots, particularly maize. Because the codon usage among monocots is similar, the genes can be used in any monocot, for example, wheat. It is further recognized that monocot optimized sequences may express in acceptable levels in dicots.

15 The plant-optimized sequence of the PAT gene was translated and compared to the native protein sequence. The protein sequence was then back-translated to nucleotide sequence using the above-described maize codon usage table. Modifications of the nucleotide sequence were not made if such modification would result in alteration of the amino acid sequence of the encoded PAT protein. The
20 basic methodology utilized to generate the monocot-optimized PAT gene sequence (moPAT) is outlined below:

a. The PAT protein amino acid sequence was "back-translated" to obtain a nucleotide sequence having those codons most frequently used in maize. A nucleotide sequence having codons reflecting
25 preferred codon usage patterns of maize and encoding the PAT protein was determined. The amino acid sequence of the protein encoded by the back-translated, modified "monocot-optimized" nucleotide sequence was identical to the amino acid sequence encoded by the native PAT nucleotide sequence.

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- b. The nucleotide sequence was further modified by removal of regions of the gene including potential RNA processing sites, degradation sequences, and premature polyadenylation sequences.
- c. Codons used <5% were avoided where possible.
- 5 d. The nucleotide sequence was further modified to delete clusters of A/T nucleotide pairs and G/C clusters having more than 10 G/C nucleotide pairs where possible. The GC content for maize genes is preferably 60-65% of the total nucleotide sequence.
- 10 e. Regions predicted to develop hairpin structures having a free energy of -12 kcal/mol were eliminated.
- f. Cloning sites comprising a restriction enzyme recognition sequence may be added or removed.
- g. Translation initiation sequence, based on a consensus from highly expressing maize genes (ACACGACACCatg), was added.
- 15 Other factors, such as those that influence transcriptional or translational initiation sizes, secondary structure of the gene or transcript, or result in modification of the poly(A) tail of the mRNA were additionally considered. A synthetic gene was then synthesized which incorporates such alterations and is shown in Figure 1.

20

EXAMPLE II. UTILIZATION OF THE moPAT GENE FOR INCREASED TRANSFORMATION EFFICIENCY

To confirm that the monocot-optimized gene was expressed in maize and produced a gene product in maize tissues, expression vectors containing the moPAT

25 gene were transformed into maize cells or tissues. Several plasmids were generated in order to test the ability of the synthetic moPAT gene to function in a monocot-optimized fashion. Two separate methods were utilized in order to determine the efficiency and level of gene expression in monocots transformed with the monocot-optimized gene constructs. One method includes transformation of monocot cells

30 with the monocot-optimized gene constructs followed by exposure of the cells to an herbicide (such as Bialaphos®, Basta, or glufosinate ammonium) to which the PAT

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gene is known to confer resistance. The number of colonies recovered following exposure to the herbicide is an indication of the ability of the monocot-optimized gene to function in maize tissues and cells. If transformation is benefited, a greater number of transformed events (herbicide-resistant colonies) would be recovered following transformation with the moPAT gene than following transformation with the PAT gene.

The data indicated that transformation of cells (comprising model or elite maize genotypes) with the I8092 (Ubi::moPAT) plasmid followed by selection on Bialaphos resulted in the generation of resistant calli. Such resistant colonies appear at an earlier time point and grow at a faster rate than those cells transformed with the PAT gene construct I6609. Furthermore, the data indicated that transformation of maize cells with the I8092 plasmid comprising the moPAT gene resulted in the isolation of a greater number of transformed events than transformation with the I6609 plasmid comprising the PAT gene (Tables 1 and 2).

RESULTS OF TRANSFORMATIONS DONE WITH moPAT:

Table 1

Experiment	I6609 clones	I8092 (moPat) clones
1	12	59
2	8	56
3	7	1
4	6	6
5	5	3
6	0	1
7	0	2
Total:	38	128

Table 2

Experiment	Construct	# Plates Shot	# Resistant Calli	Frequency
1	6609	42	800	19.0%
2	6609	42	1006	23.4%
3	8092	36	1140	31.7%

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4 8092 40 1116 27.9%

5 A second approach that was utilized to determine the ability of the moPAT gene to direct expression of the moPAT gene product in maize was detection of the PAT gene product in extracts of maize tissues. A large number of events transformed with I8092 (Ubi::moPAT) were regenerated. Table 3 gives the results of these experiments using monocots derived from transformation with either the I6609 plasmid comprising the PAT gene or the I8092 plasmid comprising the moPAT gene (ELISA values reported at pg/ μ g protein). The data indicates that the PAT gene product is detected at greater than 200 pg/ μ g total soluble protein (tsp) in a larger proportion of events transformed with the moPAT gene as compared to events transformed with the PAT gene. The data further indicated that transformation with the moPAT gene results in the recovery of a greater number of herbicide-resistant transformed events than recovery following transformation with the PAT gene.

moPAT ELISA RESULTS

Table 3

Construct	# Events	Negative	1-50	51-100	>100
	Analyzed				
16609	46	20	12	6	8
18092	84	38	5	6	35

EXAMPLE III. UTILIZATION OF A MONOCOT-OPTIMIZED GENE FOR INCREASED RECOVERY OF EVENTS TRANSFORMED WITH A NON-SELECTABLE GENE OF INTEREST

30 There is a need in the art to produce large numbers of transgenic events when developing transgenic crops. As demonstrated in the above-described example (Example II), a monocot-optimized gene may be utilized to increase recovery of transformed events following selection with a drug to which the monocot-optimized gene confers resistance. An important obstacle encountered by

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many skilled in the art is the inability to simply and accurately select for certain genes of interest. The moPAT gene functions in such a capacity, in that transformation of the moPAT gene with a gene of interest encoding a non-selectable gene product allows for selection of transformed events by selection of the transformed events in the presence of a drug.

The gene encoding a nonselectable gene product may be encoded on the same plasmid comprising the moPAT gene or may be comprised within a separate plasmid or DNA molecule. If the gene of interest is provided on a separate plasmid, then it is likely, although not absolute, that the herbicide-resistant transformed events have been co-transfected with the non-selectable gene of interest, such as the cryIA(b) gene. Similarly, if the gene of interest resides on the same plasmid comprising the moPAT gene, then it is likely that herbicide-resistant events will comprise the gene of interest in addition to the moPAT gene. Therefore, by selection of transformed events using a drug to which the moPAT gene confers resistance, the probability of isolating a transformed event expressing the gene product of the gene of interest is increased. This is extremely important when producing transgenic crops in that large numbers of transgenic events must be isolated. Thus, the optimized gene enhances the ability to recover transformed events following transformation with a non-selectable gene of interest.

EXAMPLE IV. TRANSGENIC MAIZE COMPRISING A MONOCOT-OPTIMIZED moPAT GENE

To provide a maize plant comprising a monocot-optimized gene, a transgenic maize plant is generated by transformation of a monocot-optimized gene into a maize regenerable tissue followed by regeneration of said regenerable tissue into a mature transgenic maize plant. The maize regenerable tissue is transformed with an expression vector comprising a monocot-optimized gene. Following regeneration of the mature maize plant, tissues of the transgenic plant are harvested and assayed for the presence of the monocot-optimized gene.

Monocot cells were transformed by methods known in the art. See, for example, Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA*, 85:4305-4309 and Klein

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et al. (1989) *Proc. Natl. Acad. Sci. USA*, 86:6681-6685, herein incorporated by reference. Generally, GS3 callus lines were the target issue. GS3 is a high-type II (model) corn genotype. Generally, the callus was sieved in preparation for bombardment.

5 After being bombed with particles coated with DNA at a concentration of about 0.1 μ g DNA/shot/plate, the tissue was maintained for two days on medium with no selection agent, after which the tissue was transferred to medium with a selection agent (3 μ g/liter bialaphos) to initiate the plant regeneration process.

10 Expression of the moPAT gene and its gene product confers a selective advantage to the transgenic plant. Thus, a transgenic plant is generated that has a selective advantage (herbicide resistance) over a non-transgenic plant.

EXAMPLE V. COMPARISON OF TRANSFORMATION EFFICIENCIES IN TRANSGENIC WHEAT (PAT vs moPAT).

15 PAT and moPAT were transformed into the cultivar Bobwhite (wheat) in order to determine whether the monocot-optimized CAH sequence would lead to improved transformation efficiencies in other plant species besides maize. Two experiments were conducted comparing the transformation efficiencies of the PAT gene with moPAT. Heads were harvested 12 - 14 days post anthesis, seeds sterilized
20 in 20% sodium hypochlorite for 30 min., and rinsed three times in sterile water. Immature embryos were excised and plated on MS salts, 2% sucrose, 150 mg/l asparagine, 0.5 mg/l thiamine HCl, 1.5 mg/l 2,4-D, pH 5.8, solidified with 2.5 g/l Gelrite (initiation medium). Plates were incubated in the dark at 26°C. Embryos were transferred, five days post excision, to the above medium supplemented with 0.4M
25 mannitol and cultured for four hours, then bombarded with 1 micron gold particles (0.083 μ g DNA, 650 psi).

30 Twenty hours post-bombardment, embryos were transferred from the high osmotic medium to initiation medium containing 3 mg/l Bialaphos and cultured in the dark (16/8 photo-period). The embryos were subcultured approximately every 2 weeks for 4 months. Resistant calli were placed initially on regeneration media (MS salts and vitamins, 2% sucrose, 0.5 mg/l Dicamba, 3 mg/l Bialaphos, 2.5 mg/l Gelrite), and upon shoot formation, transferred to the same medium (minus

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Dicamba) containing 5 mg/l Zeatin and transferred to light. Shoots were rooted in MS salts and vitamins at concentrations of 0.1 g/l myo-inositol, 4% sucrose, 0.7 mg/l IBA, 0.3 mg/l NAA, 1.5 g/l Gelrite. The transformation efficiency for the moPAT construct was triple that of PAT. The transformation efficiency for PAT was 0.3% and for moPAT was 0.9%, as is shown in Table 4.

PAT vs. moPAT TRANSFORMATION EFFICIENCY

Table 4

Gene	Dp#	# Embryos	# PCR+ Events	# PCR+ Events	
				with seed	Trans. Efficiency
PAT	6609	625	4	2	0.3%
moPAT	8092	568	6	5	0.9%

EXAMPLE VI. GENERATION OF A MONOCOT-OPTIMIZED CAH SEQUENCE

Cyanamide in aqueous solution or in the form of its calcium salt is used as a fertilizer in agriculture. It also can act as an effective herbicide if applied prior to sowing. The enzyme cyanamide hydratase hydrates the nitrile group of cyanamide to form urea.

Cyanamide hydratase has been purified from *Myrothecium verrucaria*. See, Maier-Greiner *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:4260-4264, herein incorporated by reference. The gene encoding cyanamide hydratase was optimized for expression in maize by the methods outlines above. Codons were altered without altering the amino acid sequence of the enzyme. The nucleic acid and amino acid sequences of the optimized gene are given in Figure 2.

EXAMPLE VII. ANALYSIS OF T1 PROGENY OF moCAH TRANSGENIC EVENTS:

To characterize the stability of the moCAH selectable marker from parent to progeny, maize cells were transformed with moCAH and successive generations were assayed for the presence of the moCAH gene. Three transgenic events were produced using the monocot-optimized cyanamide hydratase gene (moCAH) as the selectable marker. These events were confirmed at T0 plant level by Southern blot analysis. In order to confirm transgene inheritance in these events T1 plants were analyzed for the presence of the transgene using PCR and herbicide leaf painting techniques. Seeds were planted in soil in the greenhouse and plants were sampled at V4-5 leaf stage. In the first transgenic event thirty-nine T1 plants from one T0 plant were analyzed by PCR of which twenty five T1 plants were positive for the moCAH transgene. In the second transgenic event, two T0 plants were used. Fifty nine T1 plants from the first T0 were analyzed by PCR, of which thirty two were positive for the moCAH transgene. Out of fourteen T1 plants from the second T0 plant, eight T1 plants were positive for the moCAH transgene. None of the seventy-one T1 seeds germinated in the third transgenic event due to poor seed quality and mold problems.

To find out whether the inherited moCAH gene was still functional, T1 plants at V5-6 stage were leaf-painted with a 10% solution of the commercial herbicide Dormex (containing 50% cyanamide). All control non-transformed plants were susceptible to the herbicide with the painted leaf showing severe damage. Some transgenic T1 plants from both transgenic events were completely resistant to 50% cyanamide demonstrating no damage from leaf painting. In Event #2, PCR analysis showing the presence of the moCAH transgene and leaf painting results demonstrating improved resistance to cyanamide displayed a segregation pattern of approximately 1:1. These results clearly demonstrate that the moCAH gene can be used efficiently as a selectable marker to transform maize plants and that the introduced moCAH gene can be stably integrated into the maize genome and transmitted to the following generation. The DNA construct that contained the moCAH gene was arranged on the integrating vector 10675 in the order Ubi

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promoter;; moCAH gene;; PinII terminator. Sequences of the primers used for PCR confirmation of moCAH presence in the plant genome are given below.

primer 1: CTACAACCACTCCATGCGCGTGTTC

primer 2: CACATAACACACAACCTTTGATGCCCCAC

EXAMPLE VIII. COMPARISON OF TRANSFORMATION EFFICIENCIES IN TRANSGENIC WHEAT (CAH VS. moCAH).

To test whether the use of moCAH improved the transformation efficiency in other species, both CAH and moCAH were transformed into the wheat cultivar (Bobwhite). Four experiments were conducted to test CAH against moCAH transformation efficiency. Media used were as described above except that 37.5 mg/l cyanamide was substituted for Bialaphos.. No selection agent was used in the regeneration and rooting stages. The results showed a 0.0% transformation efficiency for CAH and a 0.8% transformation efficiency for moCAH.

CAH vs. moCAH TRANSFORMATION EFFICIENCY

Table 5

<u>Gene</u>	<u>Dp#</u>	<u># Embryos</u>	<u># PCR+ Events</u>	<u># PCR+ Events with seed</u>	<u>Trans. Efficiency</u>
CAH	10660	652	0	0	0%
moCAH	10675	653	5	5	0.8%

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be

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obvious that certain changes and modifications may be practiced within the scope of the appended claims.

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IN THE CLAIMS

What is claimed is:

1. A method for transforming a plant, said method comprising transforming a cell from said plant with a marker gene wherein said marker gene has been optimized for expression; and regenerating said cell into a transformed plant.
2. The method of claim 1, wherein said method comprises transforming said cell with at least one additional gene.
3. The method of claim 1, wherein said transformation is nuclear transformation.
4. The method of claim 1, wherein said transformation is chloroplast transformation.
5. The method of claim 1, wherein said plant is a monocot.
6. The method of claim 5, wherein said monocot is maize.
7. The method of claim 1, wherein said plant is a dicot.
8. The method of claim 1, wherein said marker gene is a selectable marker gene.
9. The method of claim 8, wherein said selectable marker gene is selected from a gene encoding antibiotic resistance or a gene encoding resistance to a herbicide.

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10. The method of claim 9, wherein said gene encodes phosphinothricin acetyltransferase.
11. The method of claim 9, wherein said gene encodes cyanamide hydratase.
12. The method of claim 1, wherein said marker gene is a reporter gene.
13. The method of claim 12, wherein said reporter gene is green fluorescent protein.
14. A method for increasing transformation efficiency, said method comprising transforming a cell with a marker gene wherein said marker gene has been optimized for expression in said cell; and regenerating said transformed cells into a transformed organism.
15. The method of claim 14, wherein said organism is a plant.
16. The method of claim 15, wherein said plant is a monocot.
17. The method of claim 16, wherein said monocot is maize.
18. The method of claim 14, wherein said plant is a dicot.
19. The method of claim 12, wherein said transformation efficiency is increased at least two fold.
20. The method of claim 14, wherein said transformation efficiency is increased at least five fold.

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21. The method of claim 14, wherein said transformation efficiency is increased at least ten fold.
22. The method of claim 14, wherein said method comprises transforming said cell with at least one additional gene.
23. A marker gene which has been modified to optimize expression in a plant.
24. The gene of claim 23, wherein said gene is a selectable marker gene.
25. The gene of claim 24, wherein said gene is selected from a gene encoding antibiotic resistance or a gene encoding resistance to a herbicide.
26. The gene of claim 25, wherein said gene encodes phosphinothricin acetyltransferase.
27. The gene of claim 26, wherein said gene encodes cyanamide hydratase.
28. The gene of claim 23, wherein said marker gene is a reporter gene.
29. The gene of claim 28, wherein said marker gene is green fluorescent protein.
30. A plant which has been transformed with the gene of claim 20.
31. Transformed seed from the plant of claim 30.
32. A plant which has been transformed with the gene of claim 27.

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33. Transformed seed from the plant of claim 32.
34. A plant which has been transformed with the gene of claim 29.
35. Transformed seed from the plant of claim 34.
36. The gene of claim 26, wherein said gene has the nucleotide sequence given in Figure 1.
37. The gene of claim 27, wherein said gene has the nucleotide sequence given in Figure 2.
38. A plant having stably incorporated into its genome a marker gene, wherein said marker gene has been optimized for expression.
39. The plant of claim 38, wherein said plant comprises at least one additional chimeric gene incorporated into its genome.
40. Seed of the plant of claim 38.
41. Seed of the plant of claim 39.

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FIGURE 1

MoPAT Sequence and translation:

```
1 GGATCCACAC GACACCATGT CCCCCGAGCG CCGCCCCGTC GAGATCCGCC CGGCCACCGC
61 CGCCGACATG GCCGCCGTGT GCGACATCGT GAACCACTAC ATCGAGACCT CCACCGTGAA
121 CTTCCGCACC GAGCCGCAGA CCCC GCAGGA GTGGATCGAC GACCTGGAGC GCCTCCAGGA
181 CCGCTACCCG TGGCTCGTGG CCGAGGTGGA GGGCGTGGTG GCCGGCATCG CCTACGCCGG
241 CCCGTGGAAG GCCCGCAACG CCTACGACTG GACCGTGGAG TCCACCGTGT ACGTGTCCCA
301 CCGCCACCAG CGCCTCGGCC TCGGCTCCAC CCTCTACACC CACCTCCTCA AGAGCATGGA
361 GGCCCAGGGC TTCAAGTCCG TGGTGGCCGT GATCGGCCTC CCGAACGACC CGTCCGTGCG
421 CCTCCACGAG GCCCTCGGCT ACACCGCCCG CGGCACCCTC CGCGCCGCCG GCTACAAGCA
481 CGGCGGCTGG CACGACGTCG GCTTCTGGCA GCGCGACTTC GAGCTGCCGG CCCC GCCGCG
541 CCCGGTGCGC CCGGTGACGC AGATCTGAGG TGTCGTGTTA AC
```

```
+1 MetSerProGluArgArgProValGluIleArgProAlaThrAlaAlaAspMetAlaAla
1 ATGTCCCCCGAGCGCCGCCCGTCGAGATCCGCCCGGCCACCGCCGCCGACATGGCCGCC
TACAGGGGGCTCGCGGGCGGGGCAGCTCTAGGCGGGCCGGTGCGGGCGGCTGTACCGGCCG
```

```
+1 ValCysAspIleValAsnHisTyrIleGluThrSerThrValAsnPheArgThrGluPro
61 GTGTGCGACATCGTGAACCACTACATCGAGACCTCCACCGTGAACCTCCGCACCGAGCCG
CACACGCTGTAGCACTTGGTGATGTAGCTCTGGAGGTGGCACTTGAAGGCGTGGCTCGGC
```

```
+1 GlnThrProGlnGluTrpIleAspAspLeuGluArgLeuGlnAspArgTyrProTrpLeu
121 CAGACCCCGCAGGAGTGGATCGACGACCTGGAGCGCCTCCAGGACCGCTACCCGTGGCTC
GTCTGGGGCGTCCCTACCTAGCTGCTGGACCTCGCGGAGGTCTTGCGCATGGGCACCGAG
```

```
+1 ValAlaGluValGluGlyValValAlaGlyIleAlaTyrAlaGlyProTrpLysAlaArg
181 GTGGCCGAGGTGGAGGGCGTGGTGGCCGGCATCGCCTACGCCGGCCCGTGGAAAGGCCCGC
CACCGGCTCCACCTCCCGCACCAACCGGCCGTAGCGGATGCGGCCGGGCACCTTCCGGGCG
```

```
+1 AsnAlaTyrAspTrpThrValGluSerThrValTyrValSerHisArgHisGlnArgLeu
241 AACGCCTACGACTGGACCGTGGAGTCCACCGTGACGTGTCCACCGCCACCAAGCGCTC
TTGCGGATGCTGACCTGGCACCTCAGGTGGCACATGCACAGGCTGGCGGTGCTCGCGGAG
```

```
+1 GlyLeuGlySerThrLeuTyrThrHisLeuLeuLysSerMetGluAlaGlnGlyPheLys
301 GGCCTCGGCTCCACCCTCTACACCCACCTCCTCAAGAGCATGGAGGCCAGGGCTTCAAG
```

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FIGURE 1 (cont.)

CCGGAGCCGAGGTGGGAGATGTGGGTGGAGGAGTTCTCGTACCTCCGGGTCCCGAAGTTC

+1 SerValValAlaValIleGlyLeuProAsnAspProSerValArgLeuHisGluAlaLeu
361 TCCGTGGTGGCCGTGATCGGCCTCCCGAACGACCCGTCCGTGCGCCTCCACGAGGCCCTC
AGGCACCAACCGGCACTAGCCGGAGGGCTTGCTGGGCAGGCACGCGGAGGTGCTCCGGGAG

+1 GlyTyrThrAlaArgGlyThrLeuArgAlaAlaGlyTyrLysHisGlyGlyTrpHisAsp
421 GGCTACACCGCCCGCGGCACCCCTCCGCGCCGCGGCTACAAGCACGGCGGCTGGCACGAC
CCGATGTGGCGGGCGCCGTGGGAGGCGCGGCGGCCGATGTTTCGTGCCGCCGACCGTGCTG

+1 ValGlyPheTrpGlnArgAspPheGluLeuProAlaProProArgProValArgProVal
481 GTCGGCTTCTGGCAGCGCGACTTCGAGCTGCCGGCCCCGCGCGCCCGGTGCGCCCCGGTG
CAGCCGAAGACCGTCGCGCTGAAGCTCGACGGCCGGGGCGGCGCGGGCCACGCGGGCCAC

+1 ThrGlnIle***
541 ACGCAGATCTGA
TGCGTCTAGACT

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FIGURE 2

1	TCGCGCGTTT AGCGCGCAAA	CGGTGATGAC GCCACTACTG	GGTGAAAACC CCACTTTTGG	TCTGACACAT AGACTGTGTA	GCAGCTCCCG CGTCGAGGGC
51	GAGACGGTCA CTCTGCCAGT	CAGCTTGTCT GTCGAACAGA	GTAAGCGGAT CATTCGCCTA	GCCGGGAGCA CGGCCCTCGT	GACAAGCCCG CTGTTGCGGC
101	TCAGGGCGCG AGTCCCAGCG	TCAGCGGGTG AGTCGCCCAC	TTGGCGGGTG AACC GCCCAC	TCGGGGCTGG AGCCCCGACC	CTTAACATATG GAATTGATAC
151	CGGCATCAGA GCCGTAGTCT	GCAGATTGTA CGTCTAACAT	CTGAGAGTGC GACTCTCACG	ACCATATGCG TGGTATACGC	GTGTGAAATA CACACTTTAT
201	CCGCACAGAT GGCGTGTCTA	GCGTAAGGAG CGCATTCCTC	AAAATACCGC TTTTATGGCG	ATCAGGCGCC TAGTCCGCGG	ATTCGCCATT TAAGCGGTAA
251	CAGGCTGCGC GTCCGACGCG	AACTGTTGGG TTGACAACCC	AAGGGCGATC TTCCCGCTAG	GGTGCGGGCC CCACGCCCGG	TCTTCGCTAT AGAAGCGATA
301	TACGCCAGCT ATGCGGTCTGA	GGCGAAAGGG CCGCTTTCCC	GGATGTGCTG CCTACACGAC	CAAGGCGATT GTTCCGCTAA	AAGTTGGGTA TTCAACCCAT
351	ACGCCAGGGT TGCGGTGCCA	TTTCCCAGTC AAAGGGTCAG	ACGACGTTGT TGCTGCAACA	AAAACGACGG TTTTGCTGCC	CCAGTGCCAA GGTCACGGTT
401	GCTTGCATGC CGAACGTACG	CTGCAGGTCTG GACGTCCAGC	ACTCTAGAGT TGAGATCTCA	TAACACGACA ATTGTGCTGT	CCTCACTCCC GGAGTGAGGG
451	ACGGCTTCAT TGCCGAAGTA	CAGGGTGTGTG GTCCCACAAC	GCCTCCATCT CGGAGGTAGA	GCTTGTGCGAA CGAACAGCTT	CTGCGGGATG GACGCCCTAC
501	TGGGTGGTGT ACCCACCACA	GGCACCACGG CCGTGGTGCC	CTTGTGGGAC GAACAACCTG	TCCTCCTTGC AGGAGGAACG	GCACGGTGCA CGTGCCACGT
551	GGCGAACCAG CCGCTTGGTC	GAGCACCAGC CTCGTGGTCTG	CGTGGCGCGG GCACCGCGCC	GAAGGCGGTG CTTCCGCCAC	TTGATGGAGT AACTACCTCA
601	TGCGGGTGGT ACGCCACCA	GTCGTCCACC CAGCAGGTGG	CAGGAGCCGA GTCCTCGGCT	AGTCGTGAT TCAGCAGCTA	GCCGTCGTAG CGGCAGCATC
651	GCGCCACGT CGCGGGTGCA	TGTCGTAGAG ACAGCATCTC	GGTGGCGAGC CCACCGCTCG	TGGATGAGCT ACCTACTCGA	GGCCGAGGAA CCGGCTCCTT
701	GGTGATGTTG CCACTACAAC	CCGTGACGCG GGCAGCTGCG	CGACGTCCTC GCTGCAGGAG	GTGGCGGATG CACCGCCTAC	ATGGCCTCGG TACCGGAGCC
751	CCACCGCCTC GGTGGCGGAG	CGCCTGGTCTG GCGGACCAGC	GTGGAGGAGC CACCTCCTCG	CGAGCACCT GCTCGTGGAA	GAGGACCTCC CTCCTGGAGG
801	ATCGCCTTGA TAGCGGAAC	TGCCGCCGTA ACGGCGGCAT	GATGTCGAAG CTACAGCTTC	GACATGCGGG CTGTACGCCC	TGGAGGTGAA ACCTCCACTT
851	GTAGGCCTCG CATCCGGAGC	GCGGTGCCCCA CGCCACGGGT	CGTCGTGGAG GCAGCACCTC	GAGGCAGGTG CTCCGTCCAC	AGGGCCCAGG TCCCGGGTCC

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FIGURE 2 (cont.)

901	TGGACGGGGA ACCTGCCCCCT	GAGGTCCTTG CTCCAGGAAC	GCCTGCTCCG CGGACGAGGC	GGAGGAGCCT CCTCCTCGGA	CCTGGCGATC GGACCGCTAG
951	ACGGTGCCCC TGCCACGGGG	AGTAGAACAC TCATCTTGTG	GCGCATGGAG CGCGTACCTC	TGGTTGTAGG ACCAACATCC	TCTCCGGGGA AGAGGCCCTT
1001	GAGGCGGGCC CTCCGCCCGG	TTGACGAACG AACTGCTTGC	CCTGGGCCTC GGACCCGGAG	GGCCACGAGC CCGGTGCTCG	TTGTCGGCCG AACAGCCGGC
1051	CTGGGAAGGC GACCCTTCCG	GATGTCCTCC CTACAGGAGG	ACGGAGTAGG TGCCTCATCC	AGCTGACGTC TCGACTGCAG	GCCGAGCTTG CGGCTCGAAC
1101	CCGAGGGAGT GGCTCCCTCA	CCACGATGGC GGTGCTACCG	CTTGGCGCTG GAACCGCGAC	ACGGGGACCG TGCCCTTGGC	CGGTCCAGCC GCCAGGTCGG
1151	GTTGGCCTTC CAACCGGAAG	ACCTCGGAGG TGGAGCCTCC	ACGACATGGT TGCTGTACCA	GTCGTGTGGA CAGCACACCT	TCCCCGGGTA AGGGGCCCAT
1201	CCGAATTCGT GGCTTAAGCA	AATCATGGTC TTAGTACCAG	ATAGCTGTTT TATCGACAAA	CCTGTGTGAA GGACACACTT	ATTGTTATCC TAACAATAGG
1251	GCTCACAATT CGAGTGTTAA	CCACACAACA GGTGTGTTGT	TACGAGCCGG ATGCTCGGCC	AAGCATAAAG TTCGTATTTT	TGTAAAGCCT ACATTTCTGA
1301	GGGGTGCCTA CCCCACGGAT	ATGAGTGAGC TAGTCACTCG	TAATCACAT ATTGAGTGTA	TAATTGCGTT ATTAACGCAA	GCGCTCACTG CGCGAGTGAC
1351	CCCCTTTTCC GGGCGAAAGG	AGTCGGGAAA TCAGCCCTTT	CCTGTCGTGC GGACAGCACG	CAGCTGCATT GTCGACGTAA	AATGAATCGG TTACTTAGCC
1401	CCAACGCGCG GGTTGCGCGC	GGGAGAGGCG CCCTCTCCGC	GTTTGCGTAT CAAACGCATA	TGGGCGCTCT ACCCGCGAGA	TCCGCTTCCT AGGCGAAGGA
1451	CGCTCACTGA GCGAGTGACT	CTCGCTGCGC GAGCGACGCG	TCGGTCGTTC AGCCAGCAAG	GGCTGCGGCG CCGACGCCGC	AGCGGTATCA TCGCCATAGT
1501	GCTCACTCAA CGAGTGAGTT	AGGCGGTAAT TCCGCCATTA	ACGGTTATCC TGCCAATAGG	ACAGAATCAG TGTCTTAGTC	GGGATAACGC CCCTATTGCG
1551	AGGAAAGAAC TCCTTTCTTG	ATGTGAGCAA TACACTCGTT	AAGGCCAGCA TTCCGGTCGT	AAAGGCCAGG TTTCCGGTCC	AACCGTAAAA TTGGCATTTC
1601	AGGCCGCGTT TCCGGCGCAA	GCTGGCGTTT CGACCGCAAA	TTCCATAGGC AAGGTATCCG	TCCGCCCCCC AGGCGGGGGG	TGACGAGCAT ACTGCTCGTA
1651	CACAAAAATC GTGTTTTTAT	GACGCTCAAG CTGCGAGTTC	TCAGAGGTGG AGTCTCCACC	CGAAACCCGA GCTTTGGGCT	CAGGACTATA GTCCTGATAT
1701	AAGATACCAG TTCTATGGTC	GCGTTTCCCC CGCAAAGGGG	CTGGAAGCTC GACCTTCGAG	CCTCGTGCGC GGAGCACGCG	TCTCCTGTTC AGAGGACAAG
1751	CGACCCTGCC GCTGGGACGG	GCTTACCGGA CGAATGGCCT	TACCTGTCCG ATGGACAGGC	CCTTTCTCCC GGAAAGAGGG	TTCGGGAAGC AAGCCCTTCG

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FIGURE 2 (cont.)

1801	GTGGCGCTTT CACCGCGAAA	CTCATAGCTC GAGTATCGAG	ACGCTGTAGG TGCGACATCC	TATCTCAGTT ATAGAGTCAA	CGGTGTAGGT GCCACATCCA
1851	CGTTCGCTCC GCAAGCGAGG	AAGCTGGGCT TTCGACCCGA	GTGTGCACGA CACACGTGCT	ACCCCCCGTT TGGGGGGCAA	CAGCCCCGACC GTCGGGCTGG
1901	GCTGCGCCTT CGACGCGGAA	ATCCGGTAAC TAGGCCATTG	TATCGTCTTG ATAGCAGAAC	AGTCCAACCC TCAGGTGGG	GGTAAGACAC CCATTCTGTG
			AlwNI		
1951	GACTTATCGC CTGAATAGCG	CACTGGCAGC GTGACCGTCC	AGCCACTGGT TCGGTGACCA	AACAGGATTA TTGTCCTAAT	GCAGAGCGAG CGTCTCGCTC
2001	GTATGTAGGC CATACATCCG	GGTGCTACAG CCACGATGTC	AGTTCTTGAA TCAAGAAGTT	GTGGTGGCCT CACCACCGGA	AACTACGGCT TTGATGCCGA
2051	ACACTAGAAG TGTGATCTTC	GACAGTATTT CTGTCATAAA	GGTATCTGCG CCATAGACGC	CTCTGCTGAA GAGACGACTT	GCCAGTTACC CGGTCAATGG
2101	TTCGGAAAAA AAGCCTTTTT	GAGTTGGTAG CTCAACCATC	CTCTTGATCC GAGAAGTAGG	GGCAAACAAA CCGTTTGTTT	CCACCGCTGG GGTGGCGACC
2151	TAGCGGTGGT ATCGCCACCA	TTTTTTGTTT AAAAAACAAA	GCAAGCAGCA CGTTCGTCGT	GATTACGCGC CTAATGCGCG	AGAAAAAAG TCTTTTTTTC
2201	GATCTCAAGA CTAGAGTTCT	AGATCCTTTG TCTAGGAAAC	ATCTTTTCTA TAGAAAAGAT	CGGGGTCTGA GCCCCAGACT	CGCTCAGTGG GCGAGTCACC
2251	AACGAAAACT TTGCTTTTGA	CACGTTAAGG GTGCAATTCC	GATTTTGGTC CTAAAACCAG	ATGAGATTAT TACTCTAATA	CAAAAAGGAT GTTTTTCCTA
2301	CTTCACCTAG GAAGTGGATC	ATCCTTTTAA TAGGAAAATT	ATTAAAAATG TAATTTTTAC	AAGTTTTTAA TTCAAAATT	TCAATCTAAA AGTTAGATTT
2351	GTATATATGA CATATATACT	GTAAACTTGG CATTTGAACC	TCTGACAGTT AGACTGTCAA	ACCAATGCTT TGGTTACGAA	AATCAGTGAG TTAGTCACTC
2401	GCACCTATCT CGTGGATAGA	CAGCGATCTG GTCGCTAGAC	TCTATTTTCGT AGATAAAGCA	TCATCCATAG AGTAGGTATC	TTGCCTGACT AACGGACTGA
2451	CCCCGTCGTG GGGGCAGCAC	TAGATAACTA ATCTATTGAT	CGATACCGGA GCTATGCCCT	GGGCTTACCA CCCGAATGGT	TCTGGCCCCA AGACCGGGGT
2501	GTGCTGCAAT CACGACGTTA	GATACCGCGA CTATGGCGCT	GACCCACGCT CTGGGTGCGA	CACCGGCTCC GTGGCCGAGG	AGATTTATCA TCTAAATAGT
2551	GCAATAAACC CGTTATTTGG	AGCCAGCCGG TCGGTCGGCC	AAGGGCCGAG TTCCCGGCTC	CGCAGAAGTG GCGTCTTCAC	GTCCTGCAAC CAGGACGTTG
2601	TTTATCCGCC AAATAGGGGG	TCCATCCAGT AGGTAGGTCA	CTATTAATTG GATAATTAAAC	TTGCCGGGAA AACGGCCCTT	GCTAGAGTAA CGATCTCATT
2651	GTAGTTCGCC CATCAAGCGG	AGTTAATAGT TCAATTATCA	TTGCGCAACG AACGCGTTGC	TTGTTGCCAT AACAACGGTA	TGCTACAGGC ACGATGTCCG

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FIGURE 2 (cont.)

2701	ATCGTGGTGT TAGCACCACA	CACGCTCGTC GTGCGAGCAG	GTTTGGTATG CAAACCATAC	GCTTCATTCA CGAAGTAAGT	GCTCCGGTTC CGAGGCCAAG
2751	CCAACGATCA GGTTGCTAGT	AGGCGAGTTA TCCGCTCAAT	CATGATCCCC GTACTAGGGG	CATGTTGTGC GTACAACACG	AAAAAAGCGG TTTTTTTCGCC
2801	TTAGCTCCTT AATCGAGGAA	CGGTCCTCCG GCCAGGAGGC	ATCGTTGTCA TAGCAACAGT	GAAGTAAGTT CTTCATTCAA	GGCCGCAGTG CCGGCGTCAC
2851	TTATCACTCA AATAGTGAGT	TGGTTATGGC ACCAATACCG	AGCACTGCAT TCGTGACGTA	AATTCTCTTA TTAAGAGAAT	CTGTCATGCC GACAGTACGG
2901	ATCCGTAAGA TAGGCATTCT	TGCTTTTCTG ACGAAAAGAC	TGACTGGTGA ACTGACCACT	GTACTIONACC CATGAGTTGG	AAGTCATTCT TTCAGTAAGA
2951	GAGAATAGTG CTCTTATCAC	TATGCGGCCA ATACGCCGCT	CCGAGTTGCT GGCTCAACGA	CTTGCCCGGC GAACGGGGCCG	GTCAATACGG CAGTTATGCC
3001	GATAATACCG CTATTATGGC	CGCCACATAG GCGGTGTATC	CAGAACTTTA GTCTTGAAAT	AAAGTGCTCA TTTCACGAGT	TCATTGGAAA AGTAACCTTT
3051	ACGTTCTTCG TGCAAGAAGC	GGGCGAAAAC CCCGCTTTTG	TCTCAAGGAT AGAGTTCCTA	CTTACCGCTG GAATGGCGAC	TTGAGATCCA AACTCTAGGT
3101	GTTTCGATGA CAAGCTACAT	ACCCACTCGT TGGGTGAGCA	GCACCCAACT CGTGGGTGTA	GATCTTCAGC CTAGAAGTCG	ATCTTTTACT TAGAAAATGA
3151	TTCACCAGCG AAGTGGTCGC	TTTCTGGGTG AAAGACCCAC	AGCAAAAACA TCGTTTTTGT	GGAAGGCAAA CCTTCCGTTT	ATGCCGCAAA TACGGCGTTT
3201	AAAGGGAATA TTTCCCTTAT	AGGGCGACAC TCCCGCTGTG	GGAAATGTTG CCTTTACAAC	AATACTCATA TTATGAGTAT	CTCTTCCTTT GAGAAGGAAA
3251	TTCAATATTA AAGTTATAAT	TTGAAGCATT AACTTCGTAA	TATCAGGGTT ATAGTCCCAA	ATTGTCTCAT TAACAGAGTA	GAGCGGATAC CTCGCCTATG
3301	ATATTTGAAT TATAAACTTA	GTATTTAGAA CATAAATCTT	AAATAAACAA TTTATTTGTT	ATAGGGGTTC TATCCCCAAG	CGCGCACATT GCGCGTGTAA
3351	TCCCCGAAAA AGGGGCTTTT	GTGCCACCTG CACGGTGGAC	ACGTCTAAGA TGCAGATTCT	AACCATTATT TTGGTAATAA	ATCATGACAT TAGTACTGTA
3401	TAACCTATAA ATTGGATATT	AAATAGGCGT TTTATCCGCA	ATCACGAGGC TAGTGCTCCG	CCTTTCGTC GGAAAGCAG	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/00359

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/52 C12N15/54 C12N15/82 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	RATHORE K. ET AL.: "Use of bar as a selectable marker gene and for the production of herbicide-resistant rice plants from protoplasts" PLANT MOLECULAR BIOLOGY, vol. 21, no. 5, March 1993, pages 871-884, XP002064546 see the whole document ---	1-3, 5, 8-10, 23-26, 30, 31, 38-41
X	TIAN L. ET AL.: "High level of expression of modified green fluorescent protein gene transfer in conifer tissues" IN VITRO, vol. 32, no. 4, October 1996 - December 1996, page 311 XP002064547 see the whole document ---	23, 24, 28, 29

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search

12 May 1998

Date of mailing of the international search report

27/05/1998

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 98/00359

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 96 27675 A (MEDICAL RES COUNCIL ;HASELOFF JAMES PHILLIP (AU); HODGE SARAH (GB)) 12 September 1996</p> <p>* see esp. pp. 3-8 *</p>	<p>1-3,7,8, 12,13, 23,24, 28,29</p>
X	<p>CHIU W -L ET AL: "ENGINEERED GFP AS A VITAL REPORTER IN PLANTS" CURRENT BIOLOGY, vol. 6, no. 3, 1 March 1996, pages 325-330, XP000571865</p> <p>see the whole document</p>	<p>1,3-6,8, 12-17, 23,24, 28,29, 34,35, 38,40</p>
X	<p>PANG S. ET AL.: "An improved green fluorescent protein gene as a vital marker in plants" PLANT PHYSIOLOGY, vol. 112, no. 3, November 1996, pages 893-900, XP002064548 * see esp. pp. 896/97, p. 897 first paragraph *</p>	<p>1,3,5-8, 12-19, 23,24, 28,29, 34,35, 38,40</p>

INTERNATIONAL SEARCH REPORT

information on patent family members

Internal Application No

PCT/US 98/00359

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9627675 A	12-09-1996	AU 4884396 A	23-09-1996

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February 24, 2004

VIA FACSIMILE AND AIRMAIL

250 389 2659

BARRIGAR INTELLECTUAL PROPERTY GROUP
1675 Douglas Street, Suite 290
Victoria, BC, V8W 2G5
CANADA

Re: **Notification of Transfer of Patent in Canada**
In the Name of Vertex Pharmaceuticals, Inc.
Our Reference No.: AUROBIO.020QCA
Your Reference No.: KN002/2398CA

Dear Sir or Madam:

Our firm will no longer be responsible for the prosecution and/or maintenance of the below-referenced patent application owned by Vertex Pharmaceuticals, Inc. in Canada.

Title	Application No.	Your Reference	Our Reference
MULTIWELL SCANNER AND SCANNING METHOD	2387502	KN002/2398CA	AUROBIO.020QCA

Orange County
949-760-0404

San Francisco
415-954-4114

Los Angeles
310-551-3450

Riverside
909-781-9231

San Luis Obispo
805-547-5580

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February 24, 2004

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Please direct all future correspondence to:

Lisa A. Haile, Esq.
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4365 Executive Drive, Suite 1100
San Diego, CA 92121-2133

Please acknowledge receipt of these instructions by return facsimile or by email to **instructions at kmob.com**. Thank you for your prompt attention to this matter. We look forward to your reply.

Sincerely,

Thomas R. Arno

cc: Ann Andrews, IPS

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Signed: _____ Dated: _____

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